

2016 Fall Research Symposium Abstracts

**Gustavus Adolphus College
September 16, 2016**

An Evaluation of New Technology for the Measurement of in-situ Soil Moisture and Temperature

Russell Krueger

Information about soil moisture can provide insight into plant productivity, flooding potential, and groundwater processes. Beginning in 2010, sensors to measure soil moisture and temperature were added to the measurement suite in NOAA's Climate Reference Network. New sensing technology has since been developed. With increasing failure rates of existing deployed soil sensors, alternative and less expensive sensors are desirable. With any climate monitoring network, before new sensors can be implemented, they must be compared to those currently in use to ensure that biases will not be introduced into the climate record. For this study, Acclima TDR-315 sensors (new), Stevens Hydra Probe Soil Sensors (current), and Decagon GS1 Soil Moisture Sensors (current) were installed in a test bed containing homogeneous soil. Soil moisture values were compared between sensors. The sensor values were also compared to results obtained from gravimetric methods, which is the standard for direct measurement of soil moisture. The absolute moisture values differ between sensors, but the daily changes in moisture were consistent. All of the sensors reported values significantly different from the directly measured soil moisture, but the changes in moisture were consistent between all methods. The Acclima and Hydra sensors include a soil temperature measurement, and these values were also compared in a controlled environment. The measured temperature values were comparable, but the Hydra seems to be less sensitive to changes in temperature, especially at temperatures below 15°C. The transition to the Acclima TDR-315 sensor should not introduce an unaccountable change in the data record.

Electronic Detection and Diagnosis of Health and Illness of Premature Infants

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Premature infants are particularly vulnerable to illnesses such as sepsis, which is an infection of the blood. Early diagnosis of these events can greatly reduce mortality for these babies. However, exterior signs of illness are very difficult to interpret for such weak infants and appear rather late in the infection stage. Heart rate monitoring can provide early warning of a baby's risk of contracting sepsis. Therefore, our goal is to develop a model that will best predict the risk of sepsis based on a subject's heart rate characteristics. Past research has developed a concept called the HeRO score (Heart Rate Observation), which is a measure of how likely a baby is to develop sepsis in the near future. Our research focuses on a new way of calculating the HeRO score in an attempt to provide more accurate predictions. To do so, a statistical analysis was conducted on a data set from a clinical trial, which included heart rate signals for 3,000 babies across 8 hospitals, out of which 974 sepsis events were recorded. Several multivariable logistic regression models were developed and used to create a novel HeRO score. This new method seems encouraging, as it shows an important increase of the score between periods when the babies were considered healthy and periods when they were considered sick. This could provide nurses and doctors with a more accurate estimate of the risk of impending sepsis, therefore allowing them to administer the appropriate treatment at the right time and thus save lives.

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Relationships Among Morphology, Texture, and Chemistry in Stromatolites of the Green River Formation (Eocene, Wyoming, USA)

Tanner Eischen and Lindsey Reiners

Stromatolites are among the earliest records of life on Earth and have been proposed as likely targets for biosignature exploration on other planets. They form in two principal ways: by in situ mineral precipitation and by the trapping and binding of carbonate grains. From these basic building blocks, microbialites express a wide variety of microscale textures and macroscopic forms. However, the relationships among their morphology, texture, and chemistry are poorly understood.

Lakes, especially closed-basin lakes that experience frequent changes in size and salinity, provide a good record of environmental changes because of their sensitivity to precipitation and evaporation. Likewise, the morphology, texture, and chemistry of microbialites are greatly influenced by environmental changes. The Green River Formation is a carbonate and clastic succession deposited in a complex system of interconnected mountain lakes during the Eocene Epoch. The Green River stromatolites display an array of macroscopic morphotypes across basins and even within individual beds. To probe connections between morphology and texture, samples were collected from stromatolite-rich horizons at White Mountain (Greater Green River basin) and Sand Butte (Washakie basin). Stromatolites from both localities are dominated by precipitated and grumeaux microscale textures, with subsidiary trapped-and-bound texture. Preliminary analysis using cathodoluminescence suggests distinct, lamina-scale chemical differences among fabrics, likely indicating changes in lake water conditions; however, the origin of those differences is presently unknown. To probe the relationship between texture and geochemistry, stromatolites from a single biostrome horizon (La Clede bed, Laney Member) were sampled at lamina-scale for trace element composition in conjunction with detailed petrography. This approach provides a unique opportunity to establish detailed relationships among texture, morphology, and chemistry for stromatolites at a single stratigraphic level.

Pb inventory in an ombrotrophic bog decreases over time

Erin Baumann

Peat cores were collected from the S2 ombrotrophic bog at the Marcell Experimental Forest (MEF) to determine if the Pb inventory in the bog has decreased over time. Pb concentrations in the outflow of the bog measured from 2009-2016 indicated continued mobilization and export of Pb out of the bog despite dramatic decreases in atmospheric deposition. A seminal study conducted by Urban et al. (1990) from 1981-1983 calculated a mass balance of Pb in the S2 watershed which included a Pb inventory in peat based on the approximate time frame of 1930 to 1983. We collected peat cores in 2016 to compare peat inventories of Pb over the same time range. We found that Pb inventories in the peat have decreased over time, consistent with Pb being mobilized by dissolved organic carbon (DOC) and gradually flushed out of the bog. Since 1983, DOC levels may have increased leading to further Pb mobilization and transport from the bog, but this trend is unclear. In contrast to Pb concentrations in the outflow water, upland runoff and the surface sphagnum moss layer have dramatically lower Pb concentrations compared to 1980s levels indicating fast ecosystem responses to a decrease in Pb inputs in these compartments. However, the deeper peat layers near the water table are responding more slowly to the decrease in Pb inputs and historical Pb inputs continue to be mobilized and transported from the bog. Our results would be applicable to other trace metals, such as Hg, that bind strongly to DOC. For example, a dramatic decrease in Hg deposition would not result in near-term decreases in Hg out of the bog

Laboratory Studies of O-Atom Recombination Relevant to the Earth's Upper Atmosphere

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Knowledge of the details relevant to the process of three-body O-atom recombination is critical for the study and modeling of composition, energy transfer, airglow, and transport dynamics in planetary atmospheres. Significant gaps and uncertainties exist in our understanding of the above processes, and often the relevant input from laboratory measurements is missing or outdated.

We are conducting laser-based laboratory experiments to investigate $O + O + N_2$ under conditions relevant to the Earth's mesosphere. This process is responsible for the generation of oxygen airglow. In the laboratory, an ultraviolet light pulse from a laser photoinitiates O-atom recombination in N_2 bath gas. Spectroscopic techniques are used to probe the O_2 molecules produced following recombination and subsequent relaxation in N_2 . We will present our latest laboratory results and discuss their atmospheric implications.

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Column Re-Equilibration in Hydrophilic Interaction Liquid Chromatography

Claudia Seidl, Visiting Postdoctoral Scholar

Hydrophilic interaction liquid chromatography (HILIC) is a popular method for the analysis of both small and large molecules and in most cases, it represents the best choice for the separation of hydrophilic compounds that are not sufficiently retained under reversed-phase liquid chromatography (RPLC). HILIC is becoming a routine technique in proteomic, glycomic and metabolomic research, and it is increasingly contributing to the fields of pharmaceutical, environmental and food chemistry. Moreover, the water-miscible organic rich mobile phases provide an excellent compatibility to mass spectrometric detection. The retention mechanisms in HILIC are known to be rather complex, and vary depending on stationary phase surface and mobile phase composition. Therefore, HILIC columns with different functional groups can greatly differ in selectivity, making it possible to configure a comprehensive two-dimensional system for separation of complex mixtures of hydrophilic compounds with increased peak capacity maintaining a reasonable analysis time. The ultimate goal of any chromatographic method development is to obtain acceptable resolution of all components within a realistic analysis time and the best way to achieve this using gradient elution in LC is to minimize the re-equilibration time. This work studied the run-to-run repeatability of the retention times of polar basic, acid, neutral and non-polar basic compounds separated using buffered eluents. Retention repeatability was evaluated in terms of the effect of flow rate, buffer type/concentration and stationary phase.

Understanding the Effects of Loss-of-Function of the Bipolar Disorder Risk Allele *ANK3* in Adult Mice

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Bipolar disorder is a debilitating mood disorder that affects approximately 2-4% of American adults. Current therapies are insufficient at managing the underlying cause of this disease; therefore, more work is necessary to develop novel therapeutics. Bipolar disorder is highly heritable and a large number of genetic studies have been performed to elucidate the genes contributing to this disease. Genome-wide association studies have consistently found a significant association between mutations in the *ANK3* gene and bipolar disorder. Ankyrin-G (product of the *ANK3* gene) is a scaffolding protein important for the proper formation of axon initial segments (AISs) and nodes of Ranvier, and recently has been implicated in the formation of inhibitory synapses. γ -aminobutyric acid (GABA) is the major inhibitory neurotransmitter and is essential to maintain the excitatory-inhibitory balance in the brain. Abnormalities in excitatory/inhibitory balance have been linked to bipolar disorder. Since human mutations in *ANK3* are associated with decreased mRNA expression, it is important to understand loss of function of *ANK3*. Previous studies have shown that deletion of all isoforms of ankyrin-G (*Ank3* exon 22/23 flox; nestin-Cre) or the large splice variants (*AnkG* exon 37; nestin-Cre) lead to death at postnatal day 0 or 21, respectively, precluding the study of behavior in adult animals. To overcome this limitation, our lab, in collaboration with a lab at Johns Hopkins, created an *Ank3* null mouse that survives well into adulthood (*Ank3* exon 22/23 flox; CAMKII-Cre. Hereafter, *Ank3*-KO). Interestingly, behavioral studies of the *Ank3*-KO revealed behavioral phenotypes consistent with those seen in bipolar mania, such as hyperactivity and reduced anxiety. In order to understand the molecular mechanisms underlying such behavioral phenotypes, we analyzed protein expression by western blot analysis, and found a 70% reduction in the three major isoforms of ankyrin-G in the cortex and hippocampus, when compared to wild-type mice. Imaging of coronal brain sections from the *Ank3*-KO revealed a loss of the AISs and nodes of Ranvier. In addition, we discovered a loss of GABAergic synapses on the AIS, but not on the soma, of cortical pyramidal neurons in *Ank3*-KO mice, suggesting a loss of innervation by

parvalbumin (PV) positive chandelier cells. Preliminary data revealed no significant difference in the number of PV positive cells; however, we identified a decrease in PV expression. Future studies will seek to analyze the fate of these PV positive interneurons and its effect on the entire neuronal network in hopes of creating novel therapeutics to rescue them in patients suffering from bipolar disorder.

Exploring the pathway of MYCN amplified Neuroblastoma using zebrafish

Katie Aney

Neuroblastoma is a childhood cancer that develops in the sympathoadrenal gland above the kidney and often metastasizes to cause death of the patient. It is the most common form of cancer in infants, and the survival rate is about 50%. MYCN is a well-known oncogene in neuroblastoma and acts as a transcription factor for many key genes downstream involved in tumorigenesis. Although it is known that overexpression of MYCN will lead to the development of neuroblastoma tumors, it is hard to identify therapeutic targets because the mechanism of MYCN-inducing neuroblastoma is unknown and MYCN amplification leads to the deregulation of so many genes. In Dr. Jane Zhu's lab, this mechanism is being explored using a zebrafish model system to overexpress genes and obtain tumors with genetic correlations confirmed in human tumor samples. Dr. Zhu and her colleagues have found that overexpression of MYCN synergizes with GAB2 overexpression to induce tumors at a rate five times greater than when MYCN alone is overexpressed. This is interesting considering that Gab2 alone does not induce tumorigenesis. This summer, I explored the pathways activated by Gab2. In order to gain insight into this genetic collaboration, I used RNA-seq data from neuroblastoma like tumors in zebrafish to identify key genes important in the rapid tumor formation after Gab2 overexpression. MAX, which dimerizes with MYCN to bind to DNA and induce gene expression, had one of the largest differences between the MYCN control tumors and the MYCN;GAB2 tumors. We identified MAX as a key factor in the rapid tumorigenesis, and we proposed that levels of MAX can control many of the downstream gene's expression levels by indirectly monitoring levels of MYCN and c-MYC (another neuroblastoma oncogene). Preliminary ChIP-seq, RNA and protein levels agree with a proposed mechanism where GAB2;MYCN overexpression increases the amount of downstream MAX activated through a MAP kinase pathway (Mapk1, Mapk4 and Mapk14). This in turn may be able to deregulate other oncogenes and increase the likelihood of tumorigenesis. In the future, the lab will be focusing on the protein MAX and looking into this hypothesis by creating a stable line of zebrafish with its overexpression along with MYCN to look at whether results are similar to the unexpected GAB2;MYCN tumor fish results.

Recognition of *CTF13* mRNA by Nonsense Mediated mRNA Decay in *Saccharomyces cerevisiae*

Madeline Jentink

Proteins are molecules that perform a variety of vital functions for the cell, but only when they are present at the proper concentration. Proteins are encoded by segments of DNA called genes. DNA is first copied into a more portable form, messenger RNA (mRNA), which is then converted to a sequence of amino acids, a protein. The degradation of mRNA alters its abundance and, thus, plays a central role in regulating the synthesis and thus the abundance of proteins. The nonsense mediated mRNA decay (NMD) pathway accelerates the mRNA degradation process, targeting specifically mRNAs that contain mutations resulting in incomplete protein synthesis and, thus, nonfunctional proteins. However, this pathway can also degrade wild-type mRNAs. In yeast, one such mRNA recognized by NMD is *CTF13* mRNA, which codes for a kinetochore protein. We are studying *CTF13* to understand the recognition of wild-type mRNAs by NMD. In order to determine which part of the mRNA was vital for recognition, a variety of yeast strains were made that express variants of *CTF13* mRNA. Antibodies were used to isolate the NMD protein Upf1p to determine whether *CTF13* mRNA variants were bound. *CTF13* mRNA can be detected using a polymerase chain reaction method known as quantitative PCR (qPCR). We have successfully isolated Upf1p, as shown by western blot, and have demonstrated that qPCR can quantitatively detect *CTF13* mRNA. Current efforts focus on combining these two assays in order to quantify the amount of variant *CTF13* mRNA associated with Upf1p, an indication of the degree of recognition by NMD.

Design and Construction of a New Wind Delivery System

Ben Rorem and Rochelle Widmer

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Wind energy is an increasingly necessary and viable energy source, but current wind farms are quite difficult to construct and maintain, as well as expensive to build. Sheerwind (Chaska, Minnesota) has developed a system, called Invelox, to passively increase wind speeds, allowing smaller turbines to produce comparable power to that produced by larger, utility-scale turbines. We designed a horizontal Invelox system to increase the efficiency and power output of a small, 400-watt wind turbine that will be installed on a flat-bed trailer to facilitate orientation. Aluminum bars were used to create a frame over which marine shrink wrap was stretched to create the tube. The structure will be assembled on a wooden frame, mounted on a 40-foot-long flat-bed trailer once the trailer arrives on campus. Once the construction of the system is completed, data collection will follow. The design and construction of the system will be described, as well as the hardware and software that was developed for data collection.

Rover Instrumentation: Identifying Extraterrestrial Biosignatures

Ruby Schaufler

Of the telluric planets in our solar system, Mars is the most likely to preserve evidence of life. Although Mars has a thin atmosphere today, its early history may have been habitable. The three rovers sent to Mars share a common mission, to explore whether or not Mars has or ever had a habitable surface environment. To date, these rover missions have identified several ancient environments that were potentially habitable, including: fluvial, lacustrine, and subsurface water systems.

Like their terrestrial counterparts, habitable environments on Mars have a range of potential for biosignature preservation. At a scale detectable by rovers, water-influenced sediments may preserve evidence of biological activity, including microbially-induced sedimentary structures (MISS) in clastic rocks and microbialites in chemical sedimentary rocks. Identifying these mesoscale structures and confirming whether they are microbially influenced is a challenge due to the size and subtle nature of their features.

Differentiating abiotic sedimentary structures from MISS and microbialites is a challenge even for geologists on Earth. It is even more difficult to distinguish these features for operators of a rover millions of km away. Choosing instruments that are capable of capturing the scale and detail of these features is crucial to finding biosignatures on Mars. If the wrong resolution is used, or the feature observed is too far away to capture the detail, the biosignatures will be overlooked and the mission will be unsuccessful.

Research with the Geo-Heuristic Operational Strategies Test (GHOST) team has tested various methods of traverse and collection strategy. These field tests compared efficiency and effectiveness of differing methods to locate, identify, and collect biosignatures. The field work conducted in the spring of 2016 demonstrated that mesoscale (0.1-10 mm) data is crucial when identifying MISS and microbialites. Without clear resolution on the sub-mm to cm scale, key features that allow confident assessment of biogenicity are unrecognizable. Further research is being conducted on the type of instrumentation necessary for identifying mesoscale biosignatures, specifically what resolution will be needed for distinguishing MISS and microbialites from abiogenic structures at outcrop scale.

Musks in Water: Assessing Technique for Eliminating Contaminants to Protect Native Fish and Mussels

Carston Dammann, Senior Research Student in Dr. Dwight Stoll's Lab
Research in Analytical Chemistry during the Summer of 2016

Musks, or synthetic fragrances, are compounds added to many consumer products to mask the odor of other chemicals and give the product a more pleasing smell. The most common type of musks present in the market today are polycyclic musks, specifically Galaxolide and Tonalide. These two compounds are the main musks of interest in this research project. It has been shown in other studies that these polycyclic musks are present in Wastewater Treatment Plant (WWTP) effluent, but the possible toxicity to the environment and aquatic life from these compounds and their transformation products when treated with UV light is still relatively unknown. The goal of this project is to characterize Tonalide, Galaxolide, and their transformation products using two-dimensional liquid chromatography (2D-LC) and other techniques such as online Solid-Phase Extraction (SPE). These techniques will be utilized in the Stoll Lab to investigate the presence and concentration of musks and their transformation products in WWTP effluents and influents from various locations in Minnesota. Preliminary results of the project show detectable concentrations of Tonalide, Galaxolide, and various transformation products of both polycyclic musks in effluent samples taken from the St. Peter Wastewater Treatment Plant. The use of online SPE to aid in the analysis of complex matrices, such as wastewater effluent, has also been shown to be an effective analytical technique during this project. Future directions of this project include optimizing a 2D-LC method for analyzing water samples, determining concentrations of musks and their transformation products in various effluent and influent samples, and continued collaboration with the University of St. Thomas and the University of Minnesota Crookston.

The High Five Project: Are Riparian Areas a Significant Source of Methylmercury to Rivers?

Rachel Lund

Mercury contamination of fish is a problem in Minnesota and there is a statewide advisory for consumption of fish due to mercury contamination. In this project, we studied surface water/ground water interactions in five different rivers with the highest levels of mercury in fish. One goal of this study is to identify sources of methylmercury to these river systems. Monitoring wells were installed in riparian areas in two strategic locations in each watershed. At each site, ground water samples were collected at different depths from two locations extending away from the river. Pore water samples from the river sediment and water samples from the river were also collected. The height of the ground water table was also determined at each site to determine the direction of ground water flow to the river. We have no formal conclusions yet, but the overall trends we observe are that pore water methylmercury levels are higher than the ground water methylmercury levels which are higher than the surface water methylmercury levels. This could potentially mean that methylmercury is being formed in the river sediment and transported to the river via pore water.

Oxygen Consumption During the Induction of Rapid Cold-Hardening in Isolated Muscle of Flesh Fly, *Sarcophaga bullata*

Alyssa Welle and Faculty Advisor Yuta Kawarasaki

Rapid cold-hardening (RCH) describes an extremely swift response of insects to enhance their cold tolerance. A brief exposure to a moderately low temperature dramatically increases insect survival to a subsequent cold exposure that would be lethal otherwise. In the flesh fly, *Sarcophaga bullata*, as little as 15 min at 5°C significantly improved organismal survival at -7°C from 0 to 66.7±11.1%. Previous studies have demonstrated that the induction of RCH occurs at the cellular level through calcium signaling and activation of p38 MAP kinase. In this project, we examined the changes in the oxygen consumption during the RCH induction, using isolated flight muscles of *S. bullata*. Compared to tissues that had been maintained at 5°C for 2 h, those at 5°C for 10 min, therefore during the early phase of RCH induction, exhibited significantly higher rates of oxygen consumption (1.18±0.09 vs. 2.82±0.29 $\mu\text{l O}_2 \text{ mg}^{-1} \text{ DM h}^{-1}$). When these tissues were exposed to LaCl_3 , blocker of calcium channels that has been previously described to inhibit the RCH response, their oxygen consumption rate were reduced significantly to a level similar to those that had been maintained at 5°C for 2 h. Our initial results suggest that the high rate of oxygen consumption is associated with the RCH induction, likely to meet the energetic demand of eliciting this protective response.

American Bison Cow Mate Preferences

Cassidy Coats and Madeline Aberg

Faculty Advisor: Jon Grinnell

Female American Bison (*Bison bison*) tend to mate with more dominant bulls, but it is unclear whether this is due to bull hierarchy or cow preference. During the bison mating season, which occurs from mid-July to mid-August, males compete for access to females and tend a female until she is ready to mate. While being tended, the cows exhibit behaviors such as running, walking directly away from the bull, dodging, and rejecting a chin from the bull. We observed these behaviors during ten minute focal observations of cow-bull tending pairs throughout the mating season. Our observations of these behaviors suggest that female bison do not exhibit a preference toward bulls based on their age, dominance, or condition. This finding does not support our hypothesis that cows have a choice as to which bull they mate with, and instead gives evidence for male dominance hierarchy determining which bull a cow mates with.

Seven Mile Creek Watershed

Connor Smith, Jacob Westfield, Caitlin Klaus

The Seven Mile Creek Watershed, located between St. Peter and Mankato in Southern Minnesota, is a relatively small watershed that contributes a significant amount of nitrate to the Gulf of Mexico. Much of the land in the Seven Mile Creek Watershed is used for agriculture, specifically to produce soybeans and corn. Excess water exits the soybean and corn fields through drainage tiles and carries nutrients such as nitrate and phosphorus. The nutrients then drain into the Minnesota River, followed by the Mississippi River, and are finally deposited into the Gulf of Mexico. This creates algae blooms, which makes the water susceptible to hypoxic conditions. In this way the Seven Mile Creek Watershed is responsible for the decline in shrimp and other aquatic populations. This is both an environmental crisis and an economic dilemma for the fishing industry. Working to solve this problem, farmers are implementing new methods to mitigate the amount of nitrate entering the Seven Mile Creek Watershed. It is imperative that some form of monitoring coincides with these strategies to decrease the amount of pollution, so that a definitive answer is reached as to whether or not these mitigation strategies are effective. Over the summer of 2016 three sites within the Seven Mile Creek watershed were monitored for nitrate and total suspended solids